



```

0Y 331 -ESVNLCEGDVIRIRPAGTTFLLIRONNENRHLIAKLTQITSTGGQKKEFPBAGQNPBEY 389
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 473 KESYVEGDWMTIPAGTITLYLANOE-NEDLOIVKLQPPANNCEGRDYLSAGES-QAY 530
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
0Y 390 LSTFCKELLEALNUTQTEKLGVRGQORE-GVIRASQOIRELTFRDDSERHHMIRRG 447
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 531 YSVFSDVLEALNIPDKLERITKOREREGKIVRASQDLRALSO-----RATSVRKQ 585
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
0Y 448 GESSKCPVNLNPKRPLYSNKYQAEVYKPEPYDLOMDLSEFLVANTQSGMMGPFFNTR 507
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 586 SRGRAPRTKLESQPPVNNQYQGMFEACPRDFPQLRRTDVATSVIDKQGGMVPHFNESR 645
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
0Y 508 STKVYVVAASGADYEMACPHLSGRHGGGGGK-----RHBEED-----VHYDQVBARUS 557
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 646 ATMVVYFSEGAGSFEMACPHIOSOMQGRREERBEERHMRREEBERBSGRFPERVAGRUS 705
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
0Y 558 KREALIVLAGHPVYFVSSGNENLLFAPFIMAQNMMENFLAGEBNVLODIEQANELAF 617
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 706 EGGVLTVPAGHPRIIMASPNENLTVGFGINAENNRHNFPLAGRE-NIMNELDEAKELAF 764
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
0Y 618 AAPRKEVEESFNODOSTFFPGPRHOHQOSPRSKQOQPLVLTLDVPGF 666
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 765 NVEGQAQAEIFRSQRESFTDEGP---EGGRRRRSTESPILSTILKLAGY 809
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

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RESULT      2
S22477
vicillin precursor - cacao
C:Species: Theobroma cacao (cacao)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: S22477; S22478; S18105; S22050
R:McHenry, L.; Fritz, P.J.
Plant Mol. Biol. 18, 1173-1176, 1992
A:Title: Comparison of the structure and nucleotide sequence of vicillin genes of cocoa
A:Reference number: S22477; MUID:92288309
A:Accession: S22477
A:Molecule type: DNA
A:Residues: 1-566 <MC>
A:Cross-references: EMBL:X62625
A:Accession: S22478
A:Molecule type: mRNA
A:Residues: 1-452 <MC2>
A:Cross-references: EMBL:X62626
C:Genetics:
A:Introns: 211/2; 269/3; 296/3; 391/3; 502/1
C:Superfamily: glycinin
C:Keywords: seed; storage protein
F:1-24/Domain: signal sequence #status predicted <STG>
F:25-566/Product: vicillin #status predicted <MAT>

```

[illegible]

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Db      236  VPASTGYVVSQDNQEKITIVLAPVNSQGYELFFPAONNKPESYGYGAFVELEYF 295
      403  NTOTIEKLGIVFGOOR-----EGVITIRASQEOIRELTRDSESRHHIRGCESSRGP 454
OY      296  NTOREKTEILEIEORGKRGQOOGMFRKAKPEQIRASQATSPRH---RGGE--RLA 349
Db      455  YNLFNRRLYENKYGQAEVYEPEDYRQLOMDLSVFIAANTQSSMMGPFNTSTKYVYV 514
OY      350  INLLSQSVYSNQGRCPEACPEDFSOFOQMDVAVSFKLNQCALIVPHYNSATPFVPEV 409
Db      515  ASGEADVEMACPILHSGRHGRGGRG--RHEEEDV-----HYEOVARLRSLKEALIVLA 566
OY      410  TDGYGYVMAACPHLSROSQSQSQRORRDEEESSEETGEEQOYKAPLSPDVAARA 469
Db      567  GHPVYEVSSNGENILLPAFCINAONNHENFIACERNVLOOIEPQAMELAFAPAKREEE 626
OY      470  GHAIVAFESKQDPLNAVAFGLMAQNNORIFLAGK-KVLVQRQMSSEAKELSGVPSKLVN 528
OY      627  SFNSQDQSIFFPGPRHQDQSPRSTKQOQPLVSTLDF 663
Db      529  IFNNPDESYEMFSQOQRQGRDGR---RGNPLASTLDF 562

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RESULT      3
S06398
alpha-globulin type A precursor - upland cotton
N:Alternate names: seed storage protein
C:Species: Gossypium hirsutum (upland cotton)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C:Accession: S06398
R:Chan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX
A:Reference number: S06398
A:Accession: S06398
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-605 <CHL>
A:Superfamily: glycinin
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-605/Product: alpha-globulin type A #status predicted <MAT>

```

[illegible]

[illegible]

RESULT 4  
FWCNRB  
alpha-globulin B precursor (clone C72) - upland cotton  
N:Alternate names: seed storage protein; vicilin precursor  
C:Species: *Gossypium hirsutum* (upland cotton)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999  
C:Accession: A30838; S06911  
R:Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L.  
Plant Mol. Biol. 7, 475-489, 1986  
A>Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII CLO  
A:Reference number: A30838  
A:Accession: A30838  
A:Molecule type: mRNA  
A:Residues: 1-588 <CH>  
A:Cross-references: GB:M16891; NID:g167374; PIDN:AAA33071.1; PID:g167375  
A:Experimental source: var. Coker 201  
R:Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.  
Plant Mol. Biol. 9, 533-546, 1987  
A>Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX. Se  
A:Reference number: S06398  
A:Accession: S06911  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-81 <CH>  
C:Comment: This is a seed storage protein.  
C:Superfamily: glycinin  
C:Keywords: glycoprotein; seed; storage protein  
F:1-25/Domains: signal sequence #status predicted <SIG>  
F:26-588/Product: alpha-globulin storage protein #status predicted <MAN>  
F:417/Binding site: carbohydrate (Asn) (covalent) #status predicted

[illegible]

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Db      176 EOSHNPFEHHRHSQSRPREBHGNFVYLQRAASHPLLRKINERLISEANENTFLP# 235
Oy      306 HLDADAILLVGCGALKMHHDRRESNLECCGVIRITPAFTPEYLLRNPNRNLIAKP 365
Db      236 HCDAEKIYLVNGSGTTLFTLHEKESESTNVYGVVVVPAGSVIYLANODNKERLIYAUL 295
Oy      366 LOTISTPGYAKFFPPAGGNBPDLSTFSKEILEALTOTOKLRGVFG-----QORE 418
Db      296 HRPVNNPQEFEEFPAGSQOROSYLAFRSRIIEPARNTSESQDELFGROSHRRQOO 355
Oy      419 GVIIRASOEQIRELTRDDSESRHMHIRRGGESSRGPYLENKRPLYSNKYGAUYEVRPED 478
Db      356 GMRKASQEQLRALSQEXTSPR-----EKSG-- -RFARNLLYRPRTSYNSONGREYLEACPR# 409
Oy      479 YROLQDMDLSFIANVTVOGSMMGFENTRSKIVYUVVASGADVEMACPILSGHGRGG 538
Db      410 FROLSIDINVYSALQNOGSIFEPHYNSKAFTVYVLNEGNGVEWMSPHLPQRSFEED# 469
Oy      539 KRHEEEDV-----HYEQVARLSKREAIYVLGHVVFVSSEGNELLFAFG-----I 587
Db      470 EQOODQDEEBERRSGQYRKISQSLRDIFVAVPANFVTFVASONOLRMPTGGLYONI 529
Oy      588 NAOINNHNELFGRERNVLOQIEEPAMELAFAPAKKEVEESFNODOSIIFPRGRQOOS 647
Db      530 NPDHORLETVAGKLTNH- -RQWDOSAKELAGVSSRLDELFTNNNPDESTYVS- -RQRORS 587

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RESULT 5  
S08059 alpha-globulin type B precursor (tandem 1) - upland cotton (fragment)  
N:Alternate names: seed storage protein  
C:Species: *Gossypium hirsutum* (upland cotton)  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 30-Sep-1993  
C:Accession: S08059  
R:Chian, C.A.; Borriello, K.; Kamalay, J.A.; Dure III, L.  
Plant Mol. Biol. 9, 533-546, 1987  
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX  
A:Reference number: S06398  
A:Accession: S08059  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-509 <CHL>  
A:Superfamily: glycinin

Query Match	28.9%	Score 1022.5	DB 2	Length 509
Best Local Similarity	39.3%	Pred. No. 7.8e-57		
Matches 220	Conservative 101	Mismatches 154	Indels 85	Gaps 13
QY 121	DPQOYEEGCKHCKORRETPRHMQCOQRCERREYKEKRRKQOKRYEEQOREDEEKYEEDRM	180		
Db 1	DPQRYEEGCKQEC--RQDEERKQPPCCQQRCLKRFQEQEQO-----	38		
QY 181	KEEDNRKDPQOREYEDCRRCEQOE--PRQHQQLRCRQORQHGGMNPPORG---	235		
Db 39	-----SORQFECQCHQHQQRDEKQKQCVREKREKQOE-----NPRGERE	81		
QY 236	---GSGRREEGEEEDSDMPYTFDENSLSTRRTTEGCHLSYLENPFGRSKLLRALKNRYLV	292		
Db 82	EEAEETEEEGEOESNHPFHRHSFQSRFEENGFRVYLFORFASRPDLGLGIEPRLS	141		
QY 293	LEENPNAFVLPYTHLDADAALLVYIGGRALKMIHHDNENSVNLCEGDVIRIPAGTFPLI	352		
Db 142	ILEANPNTFVLPYHHCDAKRYLVTYNGKTLTFPLTHENKESNIVGVVAKVPAGSTVYLA	201		
QY 353	NRDNNERLHAKFLTQITSPQYKEFFPAGGONPEPYLSTFSEKILLEYALNLTQTEKLRGV	412		
Db 202	NQDNKKEKLIIVLRHPVANNPQGFEEFPAGSQRSYLARSRELLPEAFNTRSQDEL	261		
QY 413	FG-----QQREGVYITASQEQIRELTRDDESESHHHIIRGGESSKGPYNLFNKRLYS	465		
Db 262	FGGRQSRROOGQGGKFRFASQEQIALSLQDZSTSP-----EKSGE--RAFAFNILSTQPYRS	315		

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OY 466 NKYGATVYKREDEYROLQDMLSTFELANVYOGSSMMGCFPNDRSKYVAVYVASSGADVEMAC 525
Db 316 NONGFEFACPERFERRODINVTYVALQJNOGSLFVPHYSKATFVLYLVEGNGYAEWMS 375
OY 526 PHLSGRHGGRCGRGRHEEDNV-----HYEQVARLSKREALVYLAGHPVVF 572
Db 376 PHLP-----KQSSYEEBEDEDEEEOQEBERRSGQYRKLRKSRDLFPVYANPVPVF 430
OY 573 VSSGNENLLLEFG-----INAAONHENFLAGERNVLOQIEQAMELAFAPDRKEEVS 627
Db 431 VASONNLRMTGFCGLYONINIPDNORIYFAGKINHY-ROMSQAEKLAFAGVSSRLVDEI 489
OY 628 FNSQDSLEFFGPPRQHQQS 647
Db 490 FNSNPOESYFVS-RQRODAS 508

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RESULT# 6
A53234
globulin-1S, GLOBIS - maize
C:Species: Zea mays (maize)
C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C:Accession: A53234; A43642
R:Belanger, F.C.; Kriz, A.L.
Genetics 129, 863-872, 1991
A:Title: Molecular basis for allelic polymorphism of the maize globulin-1 gene
A:Reference number: A53234; MUID:92090707
A:Accession: A53234
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-573 <BEL>
A:Experimental source: Inbred line Va 26
A:Note: sequence extracted from NCBI backbone (NCBIN:71280, NCBIPI:71284)
R:Kriz, A.L.
Biochem. Genet. 27, 239-251, 1989
A:Title: Characterization of embryo globulins encoded by the maize G1b genes.
A:Reference number: A43642; MUID:89374022
A:Accession: A43642
A:Status: preliminary
A:Molecule type: protein
A:Residues: 87-100 <KR1>
C:Superfamily: glycinin

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Query Match	25.6%	Score 908	DB 2	Length 573
Best Local Similarity	39.9%	Pred. No. 1.3e-49		
Matches 201	Conservative 91	Mismatches 180	Indels 32	Gaps 10

[illegible]

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QY 528 LSGRIG-----GRGGGKHHEEEDYHYRQ-----VRLRLSKREAIVYLACHPVYFVS 574
Db 384 ROSQGESEERBGKGRSRSEEESESEEEVGYGYHTIRALSLGTFVYPAGHPFVAV 443
QY 575 SGNELLIFAEGINAQNNEHFLAGRENNYLOQIEPQAMELAFAPKVEEESFNSDQS 634
Db 444 SRDSMLQIVCFEYVHADNREKVFYLAGAD-NYLQKIDRYAKALSFASKAEVDEVLGSRREK 502
QY 635 IFFPGPRO---HOQOSPSTKQOQ 655
Db 503 GFLPGPKESGHEEREDEEERE 526

```

RESULT 7  
B53234  
vicillin-like storage protein G1b1-L, embryo - maize  
N:Alternate names: globulin-IL  
C:Species: Zea mays (maize)  
C:Date: 02-May-1999 #sequence  
C:Accession: B53234; S21824  
R:Belanger, F.C.; Krile, A.L.  
Genetics 129, 863-872, 1991  
A>Title: Molecular basis for allelic polymorphism of the maize Globulin-1 gene  
A:Reference number: A53234; MUID:92090707  
A:Accession: B53234  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-582 <BEL>  
A:Cross-references: EMBL:X59083; NID:q22283; PIDN:CAA41809.1; PID:g22284  
A:Experimental source: Inbred line W6446  
A>Note: Sequence extracted from NCBI Backbone (NCBI:71285)  
C:Genetics:  
A:Gene: G1b1-L  
A:introns: 167/1; 225/3; 252/3; 349/3  
C:Superfamily: glycinin

Query Match	25.4%	Score 898	DB 2	Length 582
Best Local Similarity	39.2%	Pred. No. 5.8e-49		
Matches 197	Conservative 91	Mismatches 184	Indels 30	Gaps 9

[illegible]



```
Db 494 IIVLVINEGANIELV-----GIKEQOQROOEOPLEVKKRAELSEODIFVLPAG 545
QY 568 HPVVFVSSGNNELLLFAFGINANNHNNFLAGERNVLOOIEPOAMELAPAAKRKEVEES 627
   :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 546 YPVMV---NATSDNLFPAFGINAEKNORNLASGKNVISOIPSOVDELAPRPSAKDIENL 603
QY 628 ENSODSIFFPGRHOQOQSPSTKQOQPLVSTL 661
   :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 604 IKSOSESYPVDA--OPQKEGCKGRKGPLSTIL 635

RESULT 10
S20007
beta-conglycinin alpha chain precursor - soybean
C:Species: Glycine max (soybean)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #extl_change 31-Oct-1997
C:Accession: S20007
R:Jelleve, J.M.; Dickinson, C.D.; Dickinson, L.A.; Nielsen, N.C.
Plant Mol. Biol. 18, 259-274, 1992
A:Title: Synthesis and assembly of soybean beta-conglycinin in vitro.
A:Reference number: S20007; MUID:92119248
A:Accession: S20007
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-605 <DEL>
C:Superfamily: glycinin

Query Match 23.8%; Score 842.5; DB 2; Length 605;
Best Local Similarity 30.6%; Pred. No. 1,8e-45;
Matches 206; Conservative 143; Mismatches 223; Indels 101; Gaps 17;

QY 11 LFLSLFLSTTVS--LAESEFDROEYBCKRQCMQLETSGMRVCVSCDKRFEEDID 68
   || :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 8 LLLGLVFLASVSVSGIAYWEKENKHNKCLQSCNSERSYTNQACHARC-----N 59
QY 69 WSKYDNOEDPQTECOCCORRCROESGPROQOYCQRCKEICEEVEEYNRQD---PQOQ 125
   :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 60 LKVEKEECEEGETPRPRPRPHREPOQGE-----KEDEBDQPRPIPRPRQ 110
QY 126 YECCQKHGORRETE-PRNHQTCQQRCEERYEKKRQKRYEEOQREDEKYEERKKEED 184
   :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 111 PROEEHBOREDEWNR-----KEKKGKESSEDEDEDEBQDER--QFP 154
QY 185 NKRDPOOREYEDCRRRCOEQERPOQHCOLRCREQOROHGRGDMNPNRGSGRYEGE 244
   || :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 155 FPRPPOKE-----ERKOEDED-----EQQRESESED-----SELK 188
QY 245 EEOGDNPPYFDEKSLSTRTEEGHISVLENFGRSKLLRALKNYRLVLEPNPAFVLP 304
   :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 189 RHKNKNPFLGSRNFETLRFKNQYGRIVLQRFNQRSPOLQNLDRYILFENSKPNTLLP 248
QY 305 THLDADAILLVIGRGALKMIHNDRESYNLECGDVIRIPAGTFPILINDNNERLHIK 364
   || :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 249 NHADADYLIYILNGTALISLVNNDSDSTRLOSGDALRPPSGTTYVVPNDNNELRLIT 308
QY 365 FLQTIISPGQYKEFPFAGGONPEPYLSTFSKELLEALNTQTEKLGVP-----GQ 415
   :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 309 LAIPVKNKPFRESFPLSTEAQOSYLOGFSRNILEASDYTKFEIKVLFPSREGQOQGE 368
QY 416 QR--EGVITRASQEQRLRELTRODSERHMHIRGGSSSGCPYVLFNKRPRLYSKQOAYE 473
   || :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 369 ORLOESVIVEISKEQIRALSKRAKSSS---RKTISSEDKPFLNRSRDPYVSNKLGKFFE 424
QY 474 VPRDEYROIQDMDLSVFIANVYOGSSMMGPFNPRSTRKVVVVVASCADVEMACHLSGRIG 533
   :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 425 TPEKKNPQLRDLIDFLSYIDMNEGALLPHFNASKAIVILVINEGDANIELV----- 475
QY 534 GRGGGK-----RHEEEDVHYEQVARLSKREAIIVLAGHPVVFVSSGNNELLLFAFGIN 588
   || :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 476 ---GLKEQOQBOQOEFQPLLEVKKRYRAELSEQDIFVTPAGYVV--NATSNLNFPAIGIN 530
QY 589 AONNHENFLAGERNVLOOIEPOAMELAPAAKRKEVEESFNDSODSIFFPGRHOQOQSP 648
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Db 531 AENNORNFLAGSODNVISOIPSOVDELAPFGSAQAVEKLLKNQRESYFVDAQKKEEGN 590
QY 649 RSTKQOQPLVSTL 661
   :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 591 KGRK--GPLSTIL 601

RESULT 11
FMSYBA
beta-conglycinin alpha chain precursor - soybean
C:Species: Glycine max (soybean)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #extl_change 16-Jul-1999
C:Accession: S14681; S74124; S06714
R:Sebastiani, F.L.; Farrell, L.B.; Schuller, M.A.; Beachy, R.N.
Plant Mol. Biol. 15, 197-201, 1990
A:Title: Complete sequence of a cDNA of alpha subunit of soybean beta-conglycinin.
A:Reference number: S14681; MUID:91355860
A:Accession: S14681
A:Molecule type: mRNA
A:Residues: 1-605 <SEB>
A:Cross-references: EMBL:X17698; NID:g18535; PID:CA35691.1; PID:g18536
R:Shutov, A.D.; Kakhovskaya, I.A.; Bastiygina, A.S.; Bulmaga, V.P.; Horstmann, C.; Mu
Eur. J. Biochem. 241, 221-228, 1996
A:Title: Limited proteolysis of beta-conglycinin and glycinin, the 7S and 11S storage
A:Reference number: S74123; MUID:97054613
A:Accession: S74124
A:Molecule type: protein
A:Residues: 189-196, 'H', 198, 'N', 200, 'X', 202-203; 397-408, 'X', 410, 'X', 412-417, 'X', 419-4
A:Experimental source: seed
C:Superfamily: glycinin
C:Keywords: glycoprotein; seed; storage protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-62/Domain: propeptide #status predicted <PRO>
F:63-605/Product: beta-conglycinin alpha chain #status predicted <MAT>
F:261,517/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 23.7%; Score 840.5; DB 1; Length 605;
Best Local Similarity 30.5%; Pred. No. 2,4e-45;
Matches 205; Conservative 144; Mismatches 223; Indels 101; Gaps 17;

QY 11 LFLSLFLSTTVS--LAESEFDROEYBCKRQCMQLETSGMRVCVSCDKRFEEDID 68
   || :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 8 LLLGLVFLASVSVSGIAYWEKENKHNKCLQSCNSERSYTNQACHARC-----N 59
QY 69 WSKYDNOEDPQTECOCCORRCROESGPROQOYCQRCKEICEEVEEYNRQD---PQOQ 125
   :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 60 LKVEKEECEEGETPRPRPRPHREPOQGE-----KEDEBDQPRPIPRPRQ 110
QY 126 YECCQKHGORRETE-PRNHQTCQQRCEERYEKKRQKRYEEOQREDEKYEERKKEED 184
   :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 111 PROEEHBOREDEWNR-----KEKKGKESSEDEDEDEBQDER--QFP 154
QY 185 NKRDPOOREYEDCRRRCOEQERPOQHCOLRCREQOROHGRGDMNPNRGSGRYEGE 244
   || :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 155 FPRPPOKE-----ENNEEDED-----EQQRESESED-----SELK 188
QY 245 EEOGDNPPYFDEKSLSTRTEEGHISVLENFGRSKLLRALKNYRLVLEPNPAFVLP 304
   :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 189 RHKNKNPFLGSRNFETLRFKNQYGRIVLQRFNQRSPOLQNLDRYILFENSKPNTLLP 248
QY 305 THLDADAILLVIGRGALKMIHNDRESYNLECGDVIRIPAGTFPILINDNNERLHIK 364
   || :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 249 NHADADYLIYILNGTALISLVNNDSDSTRLOSGDALRPPSGTTYVVPNDNNELRLIT 308
QY 365 FLQTIISPGQYKEFPFAGGONPEPYLSTFSKELLEALNTQTEKLGVP-----GQ 415
   :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 309 LAIPVKNKPFRESFPLSTEAQOSYLOGFSRNILEASDYTKFEIKVLFPSREGQOQGE 368
QY 416 QR--EGVITRASQEQRLRELTRODSERHMHIRGGSSSGCPYVLFNKRPRLYSKQOAYE 473
   || :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 369 ORLOESVIVEISKEQIRALSKRAKSSS---RKTISSEDKPFLNRSRDPYVSNKLGKFFE 424
```

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QY 474 VKPEYRLOJMDLSVFLANTQSSMMGPFFNTRSTVVVVVYASGEADVENACHL5GRB 533
Db 425 ITPENKPPRLDIDLFLSTVDNNEGALLPHFNSKAIIVLIVINGDANIELV----- 475
QY 534 GRGGK-----RHHEEDVHHEGVRRARLSKREAIIVLVAIGHPVFVSSGNELLFPFGIN 588
Db 476 ----GLKEQDEQDEQDEQDEQDEQDEQDEQDEQDEQDEQDEQDEQDEQDEQDEQDEQ 530
QY 589 AONNHENFLAGRENNVLOQIEPQAMELAFAPRKVEYESFESNDQSIFFGPGRHOHQSP 648
Db 531 AENNQRNFLAGSDQNNVLSIQPSQVQELAFPGSAQAVAEKLLKQNRSEYFVDAQKKEEGN 590
QY 649 RSTKOQPLVSL 661
Db 591 KGRK--GLSLSTL 601

```

```

RESULT 12
S00566
convicillin precursor (clone pJc4) - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Aug-1999
C:Accession: S00566
R:Brown, D.; Ellis, T.H.N.; Gatehouse, J.A.
Biochem. J. 251, 717-726, 1988
A:Title: The sequence of a gene encoding convicillin from pea (Pisum sativum L.) shows th
A:Reference number: S00566; MUID:88326208
A:Accession: S00566
A:Molecule type: DNA
A:Residues: 1-571 <BOW>
A:Cross-references: EMBL:X06398; NID:920698; PIDN:CAA29695.1; PID:q113670
A:Note: Part of this sequence, including the amino end of the mature protein, was confir
C:Genetics:
A:Gene: cvcA
A:Map position: 2
A:Introns: 221/1; 279/3; 304/3; 412/3; 507/1
C:Superfamily: glycinin
F:1-38/Domain: signal sequence #status predicted <SIG>
F:29-571/Product: convicillin #status experimental <MAT>

```

Query Match	23.2%	Score 821.5;	DB 2;	Length 571;
Best Local Similarity	31.0%;	Pred. NO. 3.5e-44;		
Matches 211;	Conservative 112;	Mismatches 205;	Indels 153;	Gaps 19;

  

QY	11	LFLFLSLSTLSTYVLA	SEFDROXYE	ECKCRKQCMQ	LETSGQMRRCV	SOCDKRF	EDIM-	69
Db	12	LFLGLIITFLASCVYA	-----	NYDGSS-----	ETRVSGRER	RQGEK	EKKRHGWR	60
QY	70	SKYDNOEDPQTECCQ	CRRCRQOESG	PQOQYQCR	CKEICEE	EEEYVROR	POOQYEQC	129
Db	61	PSYKEEHE	-----					84
QY	130	QKHQRETEPRHMQT	COORCER	RYEKERKQ	KRYKEQ	REDEDE	YERKKEEDEN	189
Db	85	-----	KVQVCG-----	REMRERE-----		EDEQV	VEEWRGSRREDP	116
QY	190	QOREYEDCRRCEQ	EOEPHOQC	RCRQROHG	RGSGDM	MNPPOG	SGSGRYEEGEGSD	249
Db	117	EER-----	ARLRHEERTKDR	-----	RHQREGE	EEBERS	SSQCHHR	152
QY	250	NPYYEDERSL	RTRETEGHTSV	LENFYGR	CKLLRALK	NYALVLL	EANPAFVLT	309
Db	153	NPFLKSNKFL	TFLENENGH	IRLQRF	ERKRDLEEN	LONYLV	EXRAAPHILF	212
QY	310	DATLVIGRGAL	KMHINDRES	YNLECGDV	YIRPAG	TFPLIN	RDNNEHILAK	369
Db	213	DLIVLVNGK	ALIVLVS	NDNRNST	NLEGGDT	IKTIPAG	TTSTVLV	272
QY	370	STPGQYKEFF	PAGGONPE	PLYSTFS	CKELTEAL	MTQTE	LKGVF-----	413

[illegible]

RESULT 13

J01730

62k sucrose-binding protein precursor - soybean

C:Species: Glycine max (soybean)

C:Date: 30-Sep-1993 #sequence-Revision 30-Sep-1993 #text-change 26-Aug-1999

C:Accession: J01730

R:Grimes, H.D.; Overvoorde, P.J.; Ripp, K.; Franceschi, V.R.; Hiltz, W.D. Plant Cell 4, 1561-1574, 1992

A:Title: A 62-kD sucrose binding protein is expressed and localized in tissues active

A:Reference number: J01730; MUID:93104680

A:Accession: J01730

A:Molecule type: mRNA

A:Residues: 1-524 <GRI>

A:Cross-references: GB:L06038; NID:g1431744; PIDN:AAB03894.1; PID:g170064

C:Superfamily: glycinin

C:Keywords: sugar transport

F:1-29/Domain: signal sequence #status predicted <IG>

F:30-524/Product: 62k sucrose-binding protein #status predicted <MAT>

```

Query Match      22.8%, Score 808; DB 2; Length 524;
Best Local Similarity 33.9%; Pred. No. 2,2e+43;
Matches 194; Conservative 97; Mismatches 179; Indels 102; Gaps 17,

QY 105 RCKELCEEEELNRNRDQ--QYIQCCQKHCRRETERPHNOTCCQRCERREREKKRQ 162
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27 RCKETEVEE-----DELYTCKHQCCOQOQOYTTEGDKR--VCLOSCD-RYHRRKQERE 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 163 KRYEEOOREDEFEKYEERKKEDBNKRDPPQREYEDCRRCQEOEPQOQOQOLRCQEO 222
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 77 KOIQETREKKEE-ESRERE-----EEOEO 101
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 223 HGRGDMNPNQRGSGRYEEGEESQDPYFDE-RSLSTRPTEEGHISYLENRYGSRK 281
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 102 H-----EEDENRPIFEELKQDPETRETTGGRIRYLAKTTEKSK 140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 282 LRLALKNRLVLLLEAPNAFVLPTHLDADAILVYLGALAKMHHNDRRESYNLECGYI 341
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 141 LLOGEENRFLALEARATFPSPRHFDSEYVFNIKRAVYLGIVASESETEKLTLEPGMI 200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 342 RIPACTTYLLNRDNNEKHLA--KFLQTLSTPGQYKFEFFPAGGONPPRYLSTRSKELLE 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 HIPAGTPLYNRRNDLFLFAMLIHPIVSYSTPGKFEFFEPAGGDRDPYSASFANVLQ 260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 400 AALNTOFKLGVGOQOREGYIRASQOICBELTRDSESSHHWIRRGESGRQYNLFN 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 261 AALOTPKKLENVEDQONEGSIPIRSQOVALA-PIYKSSMNP--GGE-SKPOINFIS 316
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 460 KRPLYSNKYGALEYKRPEDRYQ--LQDDLSLVFIANYGVQSMGMPFFFTSTKVVVVASG 517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 317 KRPTISNGYGRLETVGPDDDEKSWLORLMLFTNTITORSMTIYNSHAKIALVIDG 376
OY 518 EADVEMACPHLSGRHGGRGGKHEEEDVHYEQVBARLSKREAIIVLAGHPVYVSSGN 577
Db 377 RGHLOJSCPHMS-----SRSSHSHKDKSSP-SYIRISSDLKPGWVFVYVPPHPTVIASNK 431
OY 578 ENLLFAFGINAOHNHNLFLAGERNVLOQIEPOAMELAFAADRKEVESEF----- 678
Db 432 ENLMICFEVNAADNKKFFAGKD-NIVSILDVAKELAFNYPSEVNVGVFLQREFLERK 490
OY 629 -----NSODSIFFPGRHQOOSPRS 650
Db 491 LIGRLYHLPHKDKKESFFPPFELPREGRRA 522

RESULT 14
T06459
62K sucrose-binding protein homolog - garden pea
M:Alternate names: p54 protein
C:Species: Pisum sativum (garden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C:Accession: T06459
R:Rodrigo II, M.I.
Submitted to the EMBL Data Library, February 1997
A:Reference number: Z15693
A:Accession: T06459
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-483 <ROD>
A:Cross-references: EMBL:Y11207; PIDN:CAA72090.1
A:Experimental source: var. Lincoln
C:Genetics:
A:Note: p54
C:Superfamily: glycinin

Query Match 21.7%; Score 769.5; DB 2; Length 483;
Best Local Similarity 31.4%; Pred. No. 5.2e-41;
Matches 162; Conservative 114; Mismatches 169; Indels 71; Gaps 12;

OY 135 RREPERIHQOTCOQRCERYEKKRQKRYEQOQDEDEKYEERMKEDNKRDPQOREX 194
Db 28 RKKDP-ELTTCQDCD-----MORQYDEDK----- 53
OY 195 EDCRRCEQOEPPOHQOLCREQORQHGRGDMNPORGSGRYEEGEOSDNPYF 254
Db 54 RLCMERCDYIKKQKQ-----RQKHKEH-----EEDEQOEDEENPYF 93
OY 255 DERSLSTRTEREGHISYLENFYGRSKLLRAIKNYRLVLEAPNAPFVLPTHLDADAILL 314
Db 94 EDDPFTKIDTQDGRVLLINKFNEKSKLLKNIEYGLAVLEIKANAFSLPHHYDSEAILF 153
OY 315 VIGRGALMIHHNDRESYNLECGDVIRIPAGTFGLINDNNEERLHIAKF--LQTI 371
Db 154 NIKRGITIGLVADRTERRNLEEGDLMRYPAGTPMLVNRDEMEKLYIAFHHPPSSGSA 213
OY 372 PGQYKEFPFAGGONPEPYLSTFSKEILLEALNTQTEKLGVEGQOREGVIIRASQOIRE 431
Db 214 PVNLLEFPFESAGRKPEPVNLTFSSKVLQALAKSSKGELETVDEQKGRIFKIEKEDVG 273
OY 432 LTRDSESRHHMIRRGESSRGPNLFNKRPLYSAKYGAYEVKPPDYQO-LQMDLSVF 490
Db 274 LAPKRS--LWPF--GSPFKSPFNIFSNPASFNSKFGSLFEVGPQEKSGLEGLNMLT 327
OY 491 IANVQGSMMGPFENRSTRKVVYVVASGEADVEMACPHLSGRHGGRGGRHHEEDVHYE 550
Db 328 LANITKGSSTHYNTNNAKIALVIDGELELACPHMPS-----SSNSRKOKSSISYH 382
OY 551 QVBARLSKREAIIVLAGHPVYVSSGNELLFAFGINAOHNHNLFLAGERNVLOQIEP 610
Db 383 NINAKIRPQVMFVPRAGHGFVNIASKKMLIYVCEPVNAQRNKKLALAK-KNIYSALDK 441
OY 611 QAMELAFAAPRKEVESEFNSODSIFFPGRHQO 646
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Db 442 AAKEVAFDIAAEKVDEVFERKEE-FFEPYDNERKE 476
OY 442 AAKEVAFDIAAEKVDEVFERKEE-FFEPYDNERKE 476

RESULT 15
S24756
vicillin-like storage protein precursor - white spruce
C:Species: Picea glauca (white spruce)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S24756; S18873
R:Newton, C.H.; Flinn, B.S.; Sutton, B.C.S.
Plant Mol. Biol. 20, 315-322, 1992
A:Title: Vicillin-like seed storage proteins in the gymnosperm interior spruce (Picea
A:Reference number: S24756
A:Accession: S24756
A:Molecule type: mRNA
A:Residues: 1-448 <NEW>
A:Cross-references: EMBL:X63191; NID:q20500; PIDN:CAA44873.1; PID:q20501
C:Superfamily: vicillin

Query Match 21.2%; Score 752; DB 1; Length 448;
Best Local Similarity 37.8%; Pred. No. 5.9e-40;
Matches 162; Conservative 85; Mismatches 158; Indels 24; Gaps 9;

OY 232 PORGGSGRYEEGEOSDNPYFDESLSTRFTEEGHISYLENFYGRSKLLRAIKNYRL 291
Db 34 PEYLGRGRGR-EEERENPYVHSDSFRTASSSEAGEIRALPNFGVESLLEGRKFRV 92
OY 292 VLEAPNAPFVLPTHLDADAILLIYIGRGALMIHHNDRESYNLECGDVIRIPAGTFVL 351
Db 93 TCEEMKPNVMPHRYIDATWILVTRGRGIVAYHONELVKKRLLEGDVGVPVSGHTFYL 152
OY 352 INRDNNEERLHIAKFLQTIOT-PGQYKEFPFAGGONPEPYLSTFSKEILLEALNTQTEK 410
Db 153 VNNDHNTLRISLAVRPVSTVREYOPFYAGGRNQTYVASPSDDVLAAPFTNQOLE 212
OY 411 GVFGQOREGVIIRASQOIRELTRDSESRHHMIRRG---GESSR---GPYNLFNKRPL 463
Db 213 RIRGHSQGVIIHANEQIREMR-----KRGFSAGSMKSADEHPKPFULRNQKDP 262
OY 464 YSNKYGQAAEVPRDYRQLODMDSVFIANVYOGSMKGFNTRSTKVVYVVASGEADVEM 523
Db 263 FENENGRFTIAGPKNPLIDALDVSVGLDNLPGSMTPASLNSKSTSGITVNGEGRIEM 322
OY 524 ACPHLSGRHGGRGGRHHEEDVHYEQVBARLSKREAIIVLAGHPVYVSSGNELLF 583
Db 323 ACPHL-GQHG--WSPRERGDODITYQRYWAKLRIGTSYIVPAGHPITELIASNRLQIL 379
OY 584 AFGINAOHNHNLFLAGERNVLOQIEPOAMELAFAAPR-KEYEESFNODSIFFPGRPO 642
Db 380 WFDLNRGNEROFLAK-NNVLTITEREIRQLSFNPRGEETIEVLOAKDQVILRGPR 438
OY 643 HQQSPRST 651
Db 439 RSRDEARSS 447
```

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